



#9a

SEQUENCE LISTING

<110> Huse, William D.
Watkins, Jeffry D.

<120> Tumor Specific Human Monoclonal Antibodies and Methods
of Use

<130> P-IX 2947

<140> 09/203,768

<141> 1998-12-02

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 417

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(417)

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<221> sig_peptide

<222> (1)..(57)

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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtc ctg tcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag 96
Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
20 25 30

cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc 144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
35 40 45

agt ggt tac tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg 192
Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60

gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg 240

[illegible]

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120

125

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg	96
Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg	
20 25 30	
gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct	144
Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro	
35 40 45	
ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act	192
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr	
50 55 60	
ggt atc cca gcc agg ttc agt ggc agt ggg tct ggg aca gag ttc act	240
Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr	
65 70 75 80	
ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt	288
Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys	
85 90 95	
cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag	336
Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
100 105 110	

ctg gag atc aaa cga
 Leu Glu Ile Lys Arg
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351

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 <212> PRT
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 Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
 35 40 45
 Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
 50 55 60
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 65 70 75 80
 Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
 85 90 95
 Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 100 105 110
 Leu Glu Ile Lys Arg
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<210> 5
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tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat				96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr				
20		25	30	
gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg				144
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met				
35	40	45		
gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc				192
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe				
50	55	60		
cag ggc aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac				240
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr				
65	70	75	80	
atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt				288
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys				
85	90	95		
gcg aga gaa gat agc agt ggc tgg tat cac tac tgg ggc cag gga acc				336
Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr				
100	105	110		
ctg gtc acc gtc tcc tca				354
Leu Val Thr Val Ser Ser				
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Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe			
50	55	60	

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
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<211> 333

<212> DNA

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<222> (1)..(333)

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aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30

agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60

agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa 240
 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80

gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac ccc 288
 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
 85 90 95

gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc 333
 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

<210> 8
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<400> 8
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 1 5 10 15
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 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60
 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
 85 90 95
 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110